

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Olson, Eric N.
Grant, Stephen R.
Molkentin, Jeffrey D.
- (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THERAPEUTIC
INTERVENTION IN CARDIAC HYPERTROPHY
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Houston
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(E) COUNTRY: USA
(F) ZIP: 77210
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US Unknown
(B) FILING DATE:
(C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: McMillian, Nabeela R.
(B) REGISTRATION NUMBER: P-43,363
(C) REFERENCE/DOCKET NUMBER: UTSD:548
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTATCCTTTT GTTTTCCATC CTG

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCCCTGCCTT TTCCAGCAAC GGT

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCTCCAGGAT AAAAGGCCAC GGT

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TACATTGGAA AATTTTATTA CAC

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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGGAACAA

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGGAAAAGGC

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGGATAAAAG

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 902 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Gly	Ala	Ala	Ser	Cys	Glu	Asp	Glu	Glu	Leu	Glu	Phe	Leu	Leu	Val
1				5				10					15		
Phe	Gly	Glu	Glu	Leu	Glu	Ala	Pro	Pro	Leu	Gly	Ala	Gly	Gly	Leu	Gly
			20				25					30			
Glu	Glu	Leu	Asp	Ser	Glu	Asp	Ala	Pro	Pro	Cys	Cys	Arg	Leu	Ala	Leu
		35					40					45			
Gly	Glu	Pro	Pro	Pro	Tyr	Gly	Ala	Ala	Pro	Ile	Gly	Ile	Pro	Arg	Pro
		50				55					60				
Pro	Pro	Pro	Arg	Pro	Gly	Met	His	Ser	Pro	Pro	Pro	Arg	Pro	Ala	Pro
65					70				75					80	
Ser	Pro	Gly	Thr	Trp	Glu	Ser	Gln	Pro	Ala	Arg	Ser	Val	Arg	Leu	Gly
				85				90						95	

Gly	Pro	Gly	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Gly	Arg	Val	Leu	Glu			
			100					105					110					
Cys	Pro	Ser	Ile	Arg	Ile	Thr	Ser	Ile	Ser	Pro	Thr	Pro	Glu	Pro	Pro			
		115					120					125						
Ala	Ala	Leu	Glu	Asp	Asn	Pro	Asp	Ala	Trp	Gly	Asp	Gly	Ser	Pro	Arg			
	130					135					140							
Asp	Tyr	Pro	Pro	Pro	Glu	Gly	Phe	Gly	Gly	Tyr	Arg	Glu	Ala	Gly	Ala			
145					150					155					160			
Gln	Gly	Gly	Gly	Ala	Phe	Phe	Ser	Pro	Ser	Pro	Gly	Ser	Ser	Ser	Leu			
				165					170					175				
Ser	Ser	Trp	Ser	Phe	Phe	Ser	Asp	Ala	Ser	Asp	Glu	Ala	Ala	Leu	Tyr			
			180					185					190					
Ala	Ala	Cys	Asp	Glu	Val	Glu	Ser	Glu	Leu	Asn	Glu	Ala	Ala	Ser	Arg			
		195					200					205						
Phe	Gly	Leu	Gly	Ser	Pro	Leu	Pro	Ser	Pro	Arg	Ala	Ser	Pro	Arg	Pro			
	210					215					220							
Trp	Thr	Pro	Glu	Asp	Pro	Trp	Ser	Leu	Tyr	Gly	Pro	Ser	Pro	Gly	Gly			
225					230					235					240			
Arg	Gly	Pro	Glu	Asp	Ser	Trp	Leu	Leu	Leu	Ser	Ala	Pro	Gly	Pro	Thr			
				245					250					255				
Pro	Ala	Ser	Pro	Arg	Pro	Ala	Ser	Pro	Cys	Gly	Leu	Arg	Arg	Tyr	Ser			
			260					265					270					
Ser	Ser	Gly	Thr	Pro	Ser	Ser	Ala	Ser	Pro	Ala	Leu	Ser	Arg	Arg	Gly			
		275					280					285						
Ser	Leu	Gly	Glu	Glu	Gly	Ser	Glu	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro			
	290					295					300							
Leu	Ala	Arg	Asp	Pro	Gly	Ser	Pro	Gly	Pro	Phe	Asp	Tyr	Val	Gly	Ala			
305					310					315					320			
Pro	Pro	Ala	Glu	Ser	Ile	Pro	Gln	Leu	Thr	Arg	Arg	Thr	Ser	Ser	Glu			
				325					330					335				
Gln	Ala	Val	Ala	Leu	Pro	Arg	Ser	Glu	Glu	Pro	Ala	Ser	Cys	Asn	Gly			
			340					345					350					
Leu	Leu	Pro	Leu	Gly	Ala	Glu	Glu	Ser	Val	Ala	Pro	Pro	Gly	Gly	Ser			
		355					360					365						
Arg	Lys	Glu	Val	Ala	Gly	Met	Asp	Tyr	Leu	Ala	Val	Pro	Ser	Pro	Leu			
	370					375					380							

Ala	Trp	Ser	Leu	Ala	Arg	Ile	Gly	Gly	His	Ser	Pro	Ile	Phe	Arg	Thr	385	390	395	400
Ser	Ala	Leu	Pro	Pro	Leu	Asp	Trp	Pro	Leu	Pro	Ser	Gln	Tyr	Glu	Gln	405	410	415	
Leu	Glu	Leu	Arg	Ile	Glu	Val	Gln	Pro	Arg	Ala	His	His	Arg	Ala	His	420	425	430	
Tyr	Glu	Thr	Glu	Gly	Ser	Arg	Gly	Ala	Val	Leu	Ala	Ala	Pro	Gly	Gly	435	440	445	
His	Pro	Val	Val	Leu	Leu	Leu	Gly	Tyr	Ser	Glu	Leu	Pro	Leu	Thr	Leu	450	455	460	
Gln	Met	Phe	Ile	Gly	Thr	Ala	Asp	Glu	Arg	Asn	Leu	Arg	Pro	His	Ala	465	470	475	480
Phe	Tyr	Gln	Val	His	Arg	Ile	Thr	Gly	Leu	Met	Val	Ala	Thr	Ala	Ser	485	490	495	
Tyr	Glu	Ala	Val	Val	Ser	Gly	Thr	Leu	Val	Leu	Glu	Met	Thr	Leu	Leu	500	505	510	
Pro	Glu	Asn	Asn	Met	Ala	Ala	Asn	Ile	Asp	Cys	Ala	Gly	Ile	Leu	Leu	515	520	525	
Leu	Arg	Asn	Ser	Asp	Ile	Glu	Leu	Arg	Lys	Gly	Glu	Thr	Asp	Ile	Gly	530	535	540	
Arg	Lys	Asn	Thr	Arg	Val	Arg	Leu	Val	Phe	Arg	Val	His	Val	Pro	Gln	545	550	555	560
Gly	Gly	Gly	Leu	Val	Val	Ser	Val	Gln	Ala	Ala	Ser	Val	Pro	Ile	Glu	565	570	575	
Cys	Ser	Gln	Arg	Ser	Ala	Gln	Glu	Leu	Pro	Gln	Val	Glu	Ala	Tyr	Ser	580	585	590	
Pro	Ser	Ala	Cys	Ser	Val	Arg	Gly	Gly	Glu	Glu	Leu	Val	Leu	Thr	Gly	595	600	605	
Ser	Asn	Phe	Leu	Pro	Asp	Ser	Leu	Val	Val	Phe	Ile	Glu	Arg	Gly	Pro	610	615	620	
Asp	Gly	Leu	Leu	Gln	Trp	Glu	Glu	Glu	Ala	Thr	Val	Asn	Arg	Leu	Gln	625	630	635	640
Ser	Asn	Glu	Val	Thr	Leu	Thr	Leu	Thr	Val	Pro	Glu	Tyr	Ser	Asn	Leu	645	650	655	
Arg	Val	Ser	Arg	Pro	Val	Gln	Val	Tyr	Phe	Tyr	Val	Ser	Asn	Gly	Arg	660	665	670	

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Arg	Lys	Arg	Ser	Pro	Thr	Gln	Ser	Phe	Arg	Phe	Leu	Pro	Val	Ile	Cys
		675						680					685		
Leu	Glu	Glu	Pro	Leu	Pro	Asp	Ser	Ser	Leu	Arg	Gly	Phe	Pro	Ser	Ala
		690						695				700			
Ser	Ala	Thr	Pro	Phe	Gly	Thr	Asp	Met	Asp	Phe	Ser	Pro	Pro	Arg	Pro
		705				710				715					720
Pro	Tyr	Pro	Ser	Tyr	Pro	His	Glu	Asp	Pro	Ala	Cys	Glu	Thr	Pro	Tyr
						725				730					735
Leu	Ser	Glu	Gly	Phe	Gly	Tyr	Gly	Met	Pro	Pro	Leu	Tyr	Pro	Gln	Thr
						740				745				750	
Gly	Pro	Pro	Pro	Ser	Tyr	Arg	Pro	Gly	Leu	Arg	Met	Phe	Pro	Glu	Thr
						755						765			
Arg	Gly	Thr	Thr	Gly	Cys	Ala	Gln	Pro	Pro	Ala	Val	Ser	Phe	Leu	Pro
						770					780				
Arg	Pro	Phe	Pro	Ser	Asp	Pro	Tyr	Gly	Gly	Arg	Gly	Ser	Ser	Phe	Pro
						785				795					800
Leu	Gly	Leu	Pro	Phe	Ser	Pro	Pro	Ala	Pro	Phe	Arg	Pro	Pro	Pro	Leu
						805				810				815	
Pro	Ala	Ser	Pro	Pro	Leu	Glu	Gly	Pro	Phe	Pro	Ser	Gln	Ser	Asp	Val
						820			825				830		
His	Pro	Leu	Pro	Ala	Glu	Gly	Tyr	Asn	Leu	Val	Gly	Pro	Gly	Tyr	Gly
						835			840			845			
Pro	Gly	Glu	Gly	Ala	Pro	Glu	Gln	Glu	Leu	Ser	Arg	Gly	Gly	Tyr	Ser
						850			855			860			
Ser	Gly	Phe	Arg	Asp	Ser	Val	Pro	Ile	Gln	Gly	Ile	Thr	Leu	Glu	Glu
						865				875					880
Val	Ser	Glu	Ile	Ile	Gly	Arg	Asp	Leu	Ser	Gly	Phe	Pro	Ala	Pro	Pro
						885				890				895	
Gly	Glu	Glu	Pro	Pro	Ala										
						900									

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTTCTGGAG	GGAGGCGGCA	GCGACGGAGG	AGGGGGCTTC	TCAGAGAAAG	GGAGGGAGGG	60
AGCCACCCGG	GTGAAGATAC	AGCAGCCTCC	TGAACTCCCC	CCTCCCACCC	AGGCCGGGAC	120
CTGGGGGCTC	CTGCCGGATC	CATGGGGGCG	GCCAGCTGCG	AGGATGAGGA	GCTGGAATTT	180
AAGCTGGTGT	TCGGGGAGGA	AAAGGAGGCC	CCCCCGCTGG	GCGCGGGGGG	ATTGGGGGAA	240
GAAGCTGGACT	CAGAGGATGC	CCCGCCATGC	TGCCGTCTGG	CCTTGGGAGA	GGCCCCCTCCC	300
TATGGCGCTG	CACCTATCGG	TATTCCTCCG	CCTCCACCCC	CTCGGCCTGG	CATGCATTCTG	360
CCACCGCCGC	GACCAGCCCC	CTCACCTGGC	ACCTGGGAGA	GCCAGCCCGC	CAGGTCGGTG	420
AGGCTGGGAG	GACCAGGAGG	GGGTGCTGGG	GGTGCTGGGG	GTGGCCGTGT	TCTCGAGTGT	480
CCCAGCATCC	GCATCACCTC	CATCTCTCCC	ACGCCGGAGC	CGCCAGCAGC	GCTGGAGGAC	540
AACCCTGATG	CCTGGGGGGA	CGGCTCTCCT	AGAGATTACC	CCCCACCAGA	AGGCTTTGGG	600
GGCTACAGAG	AAGCAGGGGC	CCAGGGTGGG	GGGGCCTTCT	TCAGCCCAAG	CCCTGGCAGC	660
AGCAGCCTGT	CCTCGTGGAG	CTTCTTCTCC	GATGCCTCTG	ACGAGGCAGC	CCTGTATGCA	720
GCCTGCGACG	AGGTGGAGTC	TGAGCTAAAT	GAGGCGGCCCT	CCCGCTTTGG	CCTGGGCTCC	780
CCGCTGCCCT	CGCCCCGGGC	CTCCCCCTCG	CCATGGACCC	CCGAAGATCC	CTGGAGCCTG	840
TATGGTCCAA	GGCCCCGAGG	CCGAGGGCCA	GAGGATAGCT	GGCTACTCCT	CAGTGCTCCT	900
GGGCCCACCC	CAGCCTCCCC	GCGGCCTGCC	TCTCCATGTG	GCAAGCGGCG	CTATTCCAGC	960
TCGGGAACCC	CATCTTCAGC	CTCCCCAGCT	CTGTCCCGCC	GTGGCAGCCT	GGGGGAAGAG	1020
GGGTCTGAGC	CACCTCCACC	ACCCCCATTG	CCTCTGGCCC	GGGACCCGGG	CTCCCCCTGGT	1080
CCCTTTGACT	ATGTGGGGGC	CCCACCAGCT	GAGAGCATCC	CTCAGAAGAC	ACGGCGGACT	1140
TCCAGCGAGC	AGGCAGTGGC	TCTGCCTCGG	TCTGAGGAGC	CTGCCTCATG	CAATGGGAAG	1200
CTGCCCTTGG	GAGCAGAGGA	GTCTGTGGCT	CCTCCAGGAG	GTTCCTCGAA	GGAGGTGGCT	1260
GGCATGGACT	ACCTGGCAGT	GCCCTCCCCA	CTCGCTTGGT	CCAAGGCCCG	GATTGGGGGA	1320
CACAGCCCTA	TCTTCAGGAC	CTCTGCCCTA	CCCCACTGG	ACTGGCCTCT	GGCCAGCCAA	1380
TATGAGCAGC	TGGAGCTGAG	GATCGAGGTA	CAGCCTAGAG	CCCACCACCG	GGCCACTAT	1440
GAGACAGAAG	GCAGCCGTGG	AGCTGTCAAA	GCTGCCCCTG	GCGGTCACCC	CGTAGTCAAG	1500
CTCCTAGGCT	ACAGTGAGAA	GCCACTGACC	CTACAGATGT	TCATCGGCAC	TGCAGATGAA	1560

AGGAACCTGC	GGCCTCATGC	CTTCTATCAG	GTGCACCGTA	TCACAGGCAA	GATGGTGGCC	1620
ACGGCCAGCT	ATGAAGCCGT	AGTCAGTGGC	ACCAAGGTGT	TGGAGATGAC	TCTGCTGCCT	1680
GAGAACAACA	TGGCGGCCAA	CATTGACTGC	GCGGGAATCC	TGAAGCTTCG	GAATTCAGAC	1740
ATTGAGCTTC	GGAAGGGTGA	GACGGACATC	GGGCGCAAAA	ACACACGTGT	ACGGCTGGTG	1800
TTCCGGGTAC	ACGTGCCCCA	GGGCGGCGGG	AAGGTCGTCT	CAGTACAGGC	AGCATCGGTG	1860
CCCATCGAGT	GCTCCCAGCG	CTCAGCCCAG	GAGCTGCCCC	AGGTGGAGGC	CTACAGCCCC	1920
AGTGCCCTGCT	CTGTGAGAGG	AGGCGAGGAA	CTGGTACTGA	CCGGCTCCAA	CTTCCTGCCA	1980
GACTCCAAGG	TGGTGTTCAT	TGAGAGGGGT	CCTGATGGGA	AGCTGCAATG	GGAGGAGGAG	2040
GCCACAGTGA	ACCGACTGCA	GAGCAACGAG	GTGACGCTGA	CCCTGACTGT	CCCCGAGTAC	2100
AGCAACAAGA	GGGTTTCCCG	GCCAGTCCAG	GTCTACTTTT	ATGTCTCCAA	TGGGCGGAGG	2160
AAACGCAGTC	CTACCCAGAG	TTTCAGGTTT	CTGCCTGTGA	TCTGCAAAGA	GGAGCCCCCTA	2220
CCGGACTCAT	CTCTGCGGGG	TTTCCCTTCA	GCATCGGCAA	CCCCCTTTGG	CACTGACATG	2280
GACTTCTCAC	CACCCAGGCC	CCCCTACCCC	TCCTATCCCC	ATGAAGACCC	TGCTTGCGAA	2340
ACTCCTTACC	TATCAGAAGG	CTTCGGCTAT	GGCATGCCCC	CTCTGTACCC	CCAGACGGGG	2400
CCCCCACCAT	CCTACAGACC	GGGCCTGCGG	ATGTTCCCTG	AGACTAGGGG	TACCACAGGT	2460
TGTGCCCAAC	CACCTGCAGT	TTCCTTCCTT	CCCCGCCCCT	TCCCTAGTGA	CCCGTATGGA	2520
GGGCGGGGCT	CCTCTTTCCC	CCTGGGGCTG	CCATTCTCTC	CGCCAGCCCC	CTTTCGGCCG	2580
CCTCCTCTTC	CTGCATCCCC	ACCGCTTGAA	GGCCCCTTCC	CTTCCCAGAG	TGATGTGCAT	2640
CCCCTACCTG	CTGAGGGATA	CAATAAGGTA	GGGCCAGGCT	ATGGCCCTGG	GGAGGGGGCT	2700
CCGGAGCAGG	AGAAATCCAG	GGGTGGCTAC	AGCAGCGGCT	TTCGAGACAG	TGTCCCTATC	2760
CAGGGTATCA	CGCTGGAGGA	AGTGAGTGAG	ATCATTTGGCC	GAGACCTGAG	TGGCTTCCCT	2820
GCACCTCCTG	GAGAAGAGCC	TCCTGCCTGA	ACCACGTGAA	CTGTCATCAC	CTGGCAACCC	2880
C						2881